

SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS RELATING TO THE
 PHARMACOGENETICS OF DIFFERENT GENE VARIANTS

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<140> UNKNOWN

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<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 4868

<212> DNA

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 Tyr Lys Lys Ala Leu Thr Leu Ser Asn Leu Ala Arg Lys Glu Tyr Thr
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 Val Gly Glu Thr Val Asn Leu Met Ser Val Asp Ala Gln Lys Leu Met
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 Asp Val Thr Asn Phe Met His Met Leu Trp Ser Ser Val Leu Gln Ile
 435 440 445
 Val Leu Ser Ile Phe Phe Leu Trp Arg Glu Leu Gly Pro Ser Val Leu
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 Ala Gly Val Gly Val Met Val Leu Val Ile Pro Ile Asn Ala Ile Leu
 465 470 475 480
 Ser Thr Lys Ser Lys Thr Ile Gln Val Lys Asn Met Lys Asn Lys Asp
 485 490 495
 Lys Arg Leu Lys Ile Met Asn Glu Ile Leu Ser Gly Ile Lys Ile Leu
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 Lys Tyr Phe Ala Trp Glu Pro Ser Phe Arg Asp Gln Val Gln Asn Leu

		515					520					525				
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Thr	Phe	Ser	Val	Tyr	Val	Leu	Val	Asp	Ser	Asn	Asn	Ile	Leu	Asp	Ala	
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Gln	Lys	Ala	Phe	Thr	Ser	Ile	Thr	Leu	Phe	Asn	Ile	Leu	Arg	Phe	Pro	
			580					585					590			
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Ser	Thr	Glu	Arg	Leu	Glu	Lys	Tyr	Leu	Gly	Gly	Asp	Asp	Leu	Asp	Thr	
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Ser	Ala	Ile	Arg	His	Asp	Cys	Asn	Phe	Asp	Lys	Ala	Met	Gln	Phe	Ser	
625					630					635					640	
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				645					650					655		
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			660					665					670			
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		675					680					685				
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Phe	Gly	Thr	Glu	Phe	Asn	Glu	Lys	Arg	Tyr	Gln	Gln	Val	Leu	Glu	Ala	
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Cys	Ala	Leu	Leu	Pro	Asp	Leu	Glu	Met	Leu	Pro	Gly	Gly	Asp	Leu	Ala	
			740					745					750			
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		755					760					765				
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785					790					795					800	
Asn	Lys	Val	Leu	Gly	Pro	Asn	Gly	Leu	Leu	Lys	Gly	Lys	Thr	Arg	Leu	
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			820					825					830			
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His	Thr	Gly	Pro	Glu	Glu	Ala	Thr	Val	His	Asp	Gly	Ser	Glu	Glu		
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 Ala His Phe Trp Ser Ala Phe Gly Phe Val His Ala Ser Asn Ile Leu
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 His Lys Gln Leu Leu Asn Asn Ile Leu Arg Ala Pro Met Arg Phe Phe
 1060 1065 1070
 Asp Thr Thr Pro Thr Gly Arg Ile Val Asn Arg Phe Ala Gly Asp Ile
 1075 1080 1085
 Ser Thr Val Asp Asp Thr Leu Pro Gln Ser Leu Arg Ser Trp Ile Thr
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 Cys Phe Leu Gly Ile Ile Ser Thr Leu Val Met Ile Cys Met Ala Thr
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 Pro Val Phe Thr Ile Ile Val Ile Pro Leu Gly Ile Ile Tyr Val Ser
 1125 1130 1135
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 Ser Val Thr Arg Ser Pro Ile Tyr Ser His Phe Ser Glu Thr Val Ser
 1155 1160 1165
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 1170 1175 1180
 His Asn Glu Val Arg Ile Asp Thr Asn Gln Lys Cys Val Phe Ser Trp
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 Ile Thr Ser Asn Arg Trp Leu Ala Ile Arg Leu Glu Leu Val Gly Asn
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 1220 1225 1230
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 Thr Gln Thr Leu Asn Trp Leu Val Arg Met Thr Ser Glu Ile Glu Thr
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 Asn Ile Val Ala Val Glu Arg Ile Thr Glu Tyr Thr Lys Val Glu Asn
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 Glu Ala Pro Trp Val Thr Asp Lys Arg Pro Pro Pro Asp Trp Pro Ser
 1285 1290 1295
 Lys Gly Lys Ile Gln Phe Asn Asn Tyr Gln Val Arg Tyr Arg Pro Glu
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 Lys Ile Gly Val Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Thr
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 Asp Gly Val Asp Ile Ala Ser Ile Gly Leu His Asp Leu Arg Glu Lys
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 Leu Thr Ile Ile Pro Gln Asp Pro Ile Leu Phe Ser Gly Ser Leu Arg
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 Met Asn Leu Asp Pro Phe Asn Asn Tyr Ser Asp Glu Glu Ile Trp Lys
 1395 1400 1405
 Ala Leu Glu Leu Ala His Leu Lys Ser Phe Val Ala Ser Leu Gln Leu
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 Gly Leu Ser His Glu Val Thr Glu Ala Gly Gly Asn Leu Ser Ile Gly
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 Gln Arg Gln Leu Leu Cys Leu Gly Arg Ala Leu Leu Arg Lys Ser Lys
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 Ile Leu Val Leu Asp Glu Ala Thr Ala Ala Val Asp Leu Glu Thr Asp
 1460 1465 1470
 Asn Leu Ile Gln Thr Thr Ile Gln Asn Glu Phe Ala His Cys Thr Val
 1475 1480 1485
 Ile Thr Ile Ala His Arg Leu His Thr Ile Met Asp Ser Asp Lys Val
 1490 1495 1500
 Met Val Leu Asp Asn Gly Lys Ile Ile Glu Cys Gly Ser Pro Glu Glu
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 1540 1545

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 ttttatgcaa caggaagcat aataggagat ataagacaag cacattgtaa ccttagtaga 180
 acacaatgga ataacacttt agaacagata gttaaaaaat taagagaaca atttaaaaaat 240
 aaaacaatag cttttaagca c 261

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 ttaatttctg gaaaagaagc ctaacttgtt cactacatag tcgtccttct tctctctgtg 180
 taacacttgt tggctctgtg aaataactaat ttaatggatc ctgaggttct ggaagtactt 240
 tgctgtgttc actcaagaat gtgatttgag tatgaaattc cagccagttc aactgttggt 300
 gcctattaag aaacctaata aagctccacc ttctttatct ctgaaagtga actccctgct 360
 acctttgtgg actgacagct ttttacagtc acgtgacaca gtcaaacatt aacttggtgt 420
 atcgattggg ttttgccata tatatatata agtaggagag ggccaacctc tggcaggagc 480
 aaaggcgc 488

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 ttaatttctg gaaaagaagc ctaacttgtt cactacatag tcgtccttct tctctctgtg 180
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 tgctgtgttc actcaagaat gtgatttgag tatgaaattc cagccagttc aactgttggt 300
 gcctattaag aaacctaata aagctccacc ttctttatct ctgaaagtga actccctgct 360
 acctttgtgg actgacagct ttttatagtc acgtgacaca gtcaaacatt aacttggtgt 420
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 ttaatttttg gaaaagaagc ctaacttggt cactacatag tcgtccttct tcctctctgg 180
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 tgctgtgttc actcaagaat gtgatttgag tatgaaattc cagccagttc aactgttggt 300
 gcctattaag aaacctaata aagctccacc ttctttatct ctgaaagtga actccctgct 360
 acctttgtgg actgacagct ttttatagtc acgtgacaca gtcaaacatt aacttggtgt 420
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 ttaatttttg gaaaagaagc ctaacttggt cactacatag tcgtccttct tcctctctgg 180
 taacacttgt tggctctgtg aaataactaat ttaatggatc ctgaggttct ggaagtactt 240
 tgctgtgttc actcaagaat gtgatttgag tatgaaattc cagccagttc aactgttggt 300
 gcctattaag aaacctaata aagctccacc ttctttatct ctgaaagtga actccctgct 360
 acctttgtgg actgacagct ttttatagtc acgtgacaca gtcaaacatt aacttggtgt 420
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 tctatatttc aatc atg gac caa aat caa cat ttg aat aaa aca gca gag 170
 Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu
 1 5 10
 gca caa cct tca gag aat aag aaa aca aga tac tgc aat gga ttg aag 218
 Ala Gln Pro Ser Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys
 15 20 25
 atg ttc ttg gca gct ctg tca ctc agc ttt att gct aag aca cta ggt 266
 Met Phe Leu Ala Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly
 30 35 40
 gca att att atg aaa agt tcc atc att cat ata gaa cgg aga ttt gag 314

Ala	Ile	Ile	Met	Lys	Ser	Ser	Ile	Ile	His	Ile	Glu	Arg	Arg	Phe	Glu		
45					50					55					60		
ata	tcc	tct	tct	ctt	gtt	ggt	ttt	att	gac	gga	agc	ttt	gaa	att	gga		362
Ile	Ser	Ser	Ser	Leu	Val	Gly	Phe	Ile	Asp	Gly	Ser	Phe	Glu	Ile	Gly		
				65					70					75			
aat	ttg	ctt	gtg	att	gta	ttt	gtg	agt	tac	ttt	gga	tcc	aaa	cta	cat		410
Asn	Leu	Leu	Val	Ile	Val	Phe	Val	Ser	Tyr	Phe	Gly	Ser	Lys	Leu	His		
			80					85					90				
aga	cca	aag	tta	att	gga	atc	ggt	tgt	ttc	att	atg	gga	att	gga	ggt		458
Arg	Pro	Lys	Leu	Ile	Gly	Ile	Gly	Cys	Phe	Ile	Met	Gly	Ile	Gly	Gly		
		95					100					105					
gtt	ttg	act	gct	ttg	cca	cat	ttc	ttc	atg	gga	tat	tac	agg	tat	tct		506
Val	Leu	Thr	Ala	Leu	Pro	His	Phe	Phe	Met	Gly	Tyr	Tyr	Arg	Tyr	Ser		
	110					115					120						
aaa	gaa	act	aat	atc	gat	tca	tca	gaa	aat	tca	aca	tcg	acc	tta	tcc		554
Lys	Glu	Thr	Asn	Ile	Asp	Ser	Ser	Glu	Asn	Ser	Thr	Ser	Thr	Leu	Ser		
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act	tgt	tta	att	aat	caa	att	tta	tca	ctc	aat	aga	gca	tca	cct	gag		602
Thr	Cys	Leu	Ile	Asn	Gln	Ile	Leu	Ser	Leu	Asn	Arg	Ala	Ser	Pro	Glu		
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ata	gtg	gga	aaa	ggt	tgt	tta	aag	gaa	tct	ggg	tca	tac	atg	tgg	ata		650
Ile	Val	Gly	Lys	Gly	Cys	Leu	Lys	Glu	Ser	Gly	Ser	Tyr	Met	Trp	Ile		
			160					165					170				
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Tyr	Val	Phe	Met	Gly	Asn	Met	Leu	Arg	Gly	Ile	Gly	Glu	Thr	Pro	Ile		
		175					180					185					
gta	cca	ttg	ggg	ctt	tct	tac	att	gat	gat	ttc	gct	aaa	gaa	gga	cat		746
Val	Pro	Leu	Gly	Leu	Ser	Tyr	Ile	Asp	Asp	Phe	Ala	Lys	Glu	Gly	His		
	190					195					200						
tct	tct	ttg	tat	tta	ggt	ata	ttg	aat	gca	ata	gca	atg	att	ggt	cca		794
Ser	Ser	Leu	Tyr	Leu	Gly	Ile	Leu	Asn	Ala	Ile	Ala	Met	Ile	Gly	Pro		
205					210					215					220		
atc	att	ggc	ttt	acc	ctg	gga	tct	ctg	ttt	tct	aaa	atg	tac	gtg	gat		842
Ile	Ile	Gly	Phe	Thr	Leu	Gly	Ser	Leu	Phe	Ser	Lys	Met	Tyr	Val	Asp		
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att	gga	tat	gta	gat	cta	agc	act	atc	agg	ata	act	cct	act	gat	tct		890
Ile	Gly	Tyr	Val	Asp	Leu	Ser	Thr	Ile	Arg	Ile	Thr	Pro	Thr	Asp	Ser		
			240					245					250				
cga	tgg	gtt	gga	gct	tgg	tgg	ctt	aat	ttc	ctt	gtg	tct	gga	cta	ttc		938
Arg	Trp	Val	Gly	Ala	Trp	Trp	Leu	Asn	Phe	Leu	Val	Ser	Gly	Leu	Phe		
		255					260					265					
tcc	att	att	tct	tcc	ata	cca	ttc	ttt	ttc	ttg	ccc	caa	act	cca	aat		986
Ser	Ile	Ile	Ser	Ser	Ile	Pro	Phe	Phe	Phe	Leu	Pro	Gln	Thr	Pro	Asn		
	270					275					280						
aaa	cca	caa	aaa	gaa	aga	aaa	gct	tca	ctg	tct	ttg	cat	gtg	ctg	gaa		1034
Lys	Pro	Gln	Lys	Glu	Arg	Lys	Ala	Ser	Leu	Ser	Leu	His	Val	Leu	Glu		
285					290					295					300		

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Thr Asn Asp Glu Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys	
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Asn Ile Thr Lys Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile	
320 325 330	
ctt act aat ccc ctg tat gtt atg ttt gtg ctt ttg acg ttg tta caa	1178
Leu Thr Asn Pro Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln	
335 340 345	
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Val Ser Ser Tyr Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu	
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Gln Gln Tyr Gly Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val	
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ata acc ata cct att ttt gca agt gga atg ttt tta gga gga tat atc	1322
Ile Thr Ile Pro Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile	
385 390 395	
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Ile Lys Lys Phe Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys	
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Phe Thr Ala Val Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile	
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ctc tgt gaa aac aaa tca gtt gcc gga cta acc atg acc tat gat gga	1466
Leu Cys Glu Asn Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly	
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Asn Asn Pro Val Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn	
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Ser Asp Cys Asn Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn	
465 470 475	
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Asn Gly Ile Thr Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser	
480 485 490	
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Ser Gly Asn Lys Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu	
495 500 505	
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Val Thr Gly Leu Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys	
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Pro Arg Asp Asp Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile	
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Gln Val Leu Asn Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val	
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 590 595 600

aac aac tgt ggc aca cgt ggg tca tgt agg aca tat aat tcc aca tca 1994
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 Glu Lys Asp Ile Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala
 655 660 665

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 670 675 680

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 Ala Asp Ser Glu Thr His Cys
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